A NEW SPECIES OF SCINCID LIZARD, *SAPROSCINCUS EUNGELLENSIS*, FROM MID-EASTERN QUEENSLAND

ROSS A. SADLIER, PATRICK J. COUPER, DONALD J. COLGAN, ERIC VANDERDUYS & EDWINA RICKARD

Sadlier, R.A., Couper, P.J., Colgan, D.J., Vanderduys, E. & Rickard, E. 2005 12 31: A new species of scincid lizard, *Saproscincus eungellensis*, from mid-eastern Queensland. Memoirs of the Queensland Museum **51**(2): 559-571. Brisbane. ISSN 0079-8835.

A skink, *Saproscincus eungellensis* sp. nov., is described from high altitude (>700 m) rainforests on the Clarke Range (21°01'S, 148°36'S) in mid-eastern Queensland. It is most similar in morphology, behavior, and habitat preference to several species (*S. challengeri*, *S. spectabilis*, and *S. rosei* - the '*challengeri*' group) from the moist forests of northeastern New South Wales and southeastern Queensland, approximately 800km or more to the south, and in appearance most closely resembles *S. challengeri*, a species restricted to the Border Ranges region. Its large size, differences in scalation, and genetic data, readily distinguish *S. eungellensis* sp. nov. from these species. Genetic data from two independent mitochondrial DNA studies support the close relationship of *Saproscincus eungellensis* sp. nov. with the southern taxa, but give different interpretations of intraspecific relationships between these species. The combined 12S ribosomal RNA and Cytochrome *b* data presented here clearly identifies *Saproscincus eungellensis* sp. nov. as a member of the '*challengeri*' group, and to a lesser degree as basal to the other species in the group. The description of this species brings the number of reptiles endemic to the Mackay Coast to eight (*Phyllurus championae, P. isis, P. nepthys, P. ossa, Eulamprus amplus, E. luteilateralis, Saproscincus eungellensis* sp. nov. and *S. hannahae*). Of these, *P. nepthys, E. luteilateralis* and *S. eungellensis* sp. nov. are confined to the Clarke Range. Because of its narrowly-restricted distribution (< 500km^2) and its reliance upon high altitude rainforests, *S. eungellensis* sp. nov faces a projected decline in its area of occupancy through processes relating to global warming and interactions from other threatening processes. It satisfies the criteria for an Endangered listing under the Queensland Nature Conservation Act 1992, Nature Conservation (Wildlife) Regulation 1994. ☐ Saproscincus eungellensis, *new species*, *Scincidae, rainforests, Queensland.*

Ross Sadlier, Don Colgan & Edwina Rickard, Australian Museum, 6 College Street, Sydney 2000, NSW; Patrick Couper, Queensland Museum, PO Box 3300, South Brisbane 4101, Queensland; Eric Vanderduys, Environmental Protection Agency, PO Box 5391, Townsville MC, 4810; 11 July 2005.

Research into the lizards in eastern Australian rainforests, in particular the gekkonids *Saltuarius* and *Phyllurus* and the scincid *Saproscincus*, has led to discovery of several new species in the past decade. Some of these are the result of recent field collections made in areas not before adequately investigated (Couper et al., 2000; Hoskin et al., 2003), the recognition of distinct sibling taxa from museum based collections (Couper & Keim, 1998), or a combination of the two (Couper et al., 1993).

In the 1970's a series of surveys of major rainforest blocks in Queensland and areas of northern NSW (Broadbent & Clark, 1976) investigated several sites in mid-eastern Queensland including the high elevation forests of Eungella (20°55'S, 148°30'E) in the Clarke Range west of Mackay. Voucher collections were lodged in the Australian and Queensland Museums. Amongst this material were two specimens of a moderate-sized skink assignable to *Saproscincus*, but not readily allocated to any existing species.

Acquisition of additional specimens allows assessment of morphological variation within the new taxon and variation between it and other species of *Saproscincus*. Tissue samples obtained from these specimens have facilitated comparative intrageneric genetic studies that provide an independent assessment of the status of the species. The results of these studies identify the large *Saproscincus* from the Eungella area as a new species, whose closest relatives are a lineage of three species, the '*challengeri*' group (*S. challengeri*, *S. spectabilis*, and *S. rosei*) from SE Qld and NE NSW.

MATERIALS AND METHODS

Abbreviations: QM=Queensland Museum, Brisbane; AMS=Australian Museum, Sydney.

The following suite of morphological characters were scored for each specimen where possible: snout to vent length (SVL) - measured from tip of snout to caudal edge of anal scales; axilla to groin distance - measured from middle of base of forelimb to base of hindlimb; forelimb to snout length - measured from tip of snout to middle of base of forelimb; hindlimb length - measured from middle of base of hindlimb to tip of fourth toe including claw; tail length - measured from caudal edge of anal scales to tip of tail, the degree to which the original tail is present being determined by X-ray. Body measurements (axilla to groin, forelimb to snout, hindlimb) are for adult specimens, and are expressed as percentages of snout to vent length in the species accounts. Specimens were regarded as sexually mature (adults) if they showed signs of reproductive maturity (presence of enlarged yolked ovarian follicles or eggs in females, and presence of enlarged testes and distinctive colouration in males) and/or if they were within the size class as determined by the minimum size at reproductive maturity.

Head scalation generally follows Taylor (1935). Midbody scale rows - number of longitudinal scale rows around body counted midway between axilla and groin. Paravertebral scales - number of scales in a paravertebral row from first scale posterior of parietal scale to last scale at the level of vent opening. Fourth finger and toe scales - number of dorsal scales on fourth digit of hand and foot, distal scale contains claw, basal scale of fourth finger is usually present as a single large scale common to the base of the fourth finger, and basal scale of fourth toe broadly contacts basal scale of adjacent third toe. Fourth finger and toe lamellae - number of ventral scales on fourth digit of hand and foot, distal scale contains claw and basal scale is the most proximal largely undivided scale at a point level with intersection of third and fourth digits. Bilateral scalation characters were scored on both sides. Individual values determined the range and were used in determining percentage frequencies. The mean value of the two individual vales was used in determining the overall mean value for each species, and deviation from the mean value is standard deviation.

Phalangeal formula and the number of presacral and postsacral vertebrae was assessed by X-ray.

DNA EXTRACTION AND SEQUENCING. Specimens used and the corresponding registration numbers are listed in Appendix. DNA was extracted from a small amount of tissue (30–50mg) by the CTAB method of Saghai-Maroof et al. (1984) or the AMRESCO RapidGene™ Genomic DNA Purification Kit according to manufacturer's instructions. The DNA was resuspended in 100-200µl of TE buffer (depending on pellet size) and 3µl of this preparation was run on a 1% agarose gel containing ethidium bromide and UV-visualised. Where the DNA was low in abundance it was used undiluted. Otherwise, the DNA was diluted between 1 in 10 and 1 in 40 with water before use.

The primer pairs used and segment abbreviations used herein are as follows, with ambiguities written in standard IUB codes:

Cytochrome *b* (Cytb) was generally amplified using the Kocher et al. (1989) 'universal' primers):

CytbF: 5'-AAA AAG CTT CCA TCC AAC ATC TCA GCA TGA TGA AA-3' and

CytbR: 5'-AAA CTG CAG CCC CTC AGA ATG ATA TTT GTC CTC A-3'

Specimens that could not be amplified with this pair were amplified with the primers:

Cytb(skink)F: 5'-TGC CTC ATC ATW CAA GTA CTY AC-3'

Cytb(skink)R: 5'- GTG AGG GTG GCR TTR TCT ACT G-3'

These were designed for this study.

12S ribosomal DNA (12S) was also amplified using primers designed by Kocher et al. (1989):

12SF (= L1091): 5'-AAA AAG CTT CAA ACT GGG ATT AGA TAC CCC-3'

12SR (=H1478): 5'-TGA CTG CAG AGG GTG ACG GGC GGT GTG T-3'

PCR was performed using 1.0 Units of QIAGEN (Venlo, The Netherlands) thermostable DNA polymerase, in the manufacturer's buffer (1X concentration), 0.05 mM dNTPs, 3.5 mM $MgCl_2$ and 12.5 pmol of each primer in a total reaction made up to a volume of 49µl with water. 1µL of diluted DNA was added. Negative controls (without DNA) were included in each reaction array. To optimise PCR products, annealing temperatures and times, and $MgCl_2$ concentration were varied. For Cytb and

CytB-skink primer pairs, the cycling profile was as follows: (95°C for 5 min, 50°C for1 min, 72°C for 1 min) for one cycle, (95°C for 30 sec, 50°C for 1 min, 72°C for 1 min) for 32 cycles and 72°C for 3 min for the final cycle. A similar profile was conducted for 12S except that the annealing temperature was increased to 52°C. Reaction products were resolved on 2% agarose gels. All single band products were purified using AMPURE magnetic beads (Agencourt) processed by a liquid handling system (Corbett Engineering CAS-3800).

Products were sequenced in both directions on an Applied Biosystems (ABI)® 310 DNA Sequencer using the DyeDeoxy™ Terminator sequencing method according to the manufacturer's protocol except that reactions were scaled down to 10µl using 2µl Big Dye version 2.0 reaction mix (Applied Biosystems) Sequencing reactions were purified using CleanSeq magnetic beads (Agencourt) on the Corbett liquid handler.

SEQUENCE ALIGNMENT AND PHYLOGENETIC ANALYSIS. Consensus sequences for each taxon were generated by assembling forward and reverse sequences using Sequencher (Gene Codes). Sequences were aligned using default values for parameters in CLUSTAL X (Thompson et al., 1994). There were no areas of uncertain alignment in either of the genes.

Average genetic distances between groups of sequences were determined by MEGA 3.1 (Kumar et al., 2004). Values for the Kimura two-parameter metric are reported here.

Maximum parsimony analyses were carried out for each data set separately and in combination, using PAUP* 4.0. version b10 (Swofford, 2001) with heuristic searches for unweighted analysis of the genes either singly or combined (200 replications of random stepwise addition of taxa were conducted with no more than 200 trees greater than length 300 kept in each replicate). Analyses were performed using the tree-bisection-reconnection (TBR) branch-swapping algorithm. MULPARS was in effect. The steepest descent option was not enforced and accelerated transformation for character optimisation was assumed. Zero length branches were collapsed to give polytomies. Gaps were treated as unknown in all analyses.

For maximum likelihood analyses, the GTR+I+G model was assumed with the following settings determined by the Akaike Information Criterion as implemented in MODELTEST (Posada and Crandall, 1998). The number of substitution types was six, with substitution rate-matrix parameters estimated as (A to C: 19299.9316, A to G: 123654.4922; A to T: 21759.3789; C to G: 10480.1836; C to T: 203837.5469; and G to T: 1.0000). The assumed nucleotide frequencies were (A: 0.3206 C: 0.2823 G: 0.1775 T: 0.2196). To accommodate among-site rate variation the proportion of invariable sites was estimated as 0.5269 and the distribution of rates at variable sites assumed to follow the gamma distribution with $\alpha = 0.8790$ with the number of rate categories set at four. Other parameters took the default values in PAUP 4.0.

Bayesian analyses were conducted using MrBayes (Version 3.01) (Huelsenbeck & Ronquist, 2001). Markov Chains were run for 400,000 steps and the first 60,000 were discarded (after examination of topology probabilities) to allow for convergence. Four differentially heated chains were run simultaneously. Topologies were sampled every 100 generations. Likelihood settings were determined during the run. These were: (i) base frequencies; (ii) the independent rates of the six substitution types; (iii) the proportion of invariable sites; and (iv) the shape parameter of the gamma distribution that was assumed for variation in the rate of substitution between nucleotide positions in the alignment. Parameter estimation was conducted separately for each gene (and each codon position within coding sequences) using a character partition and the "unlink" command in MrBayes.

The 12S rDNA dataset comprised 52 sequences from *Saproscincus* plus five outgroup sequences from the skinks *Lampropholis* (2), *Harrisoniascincus* (1), and *Carlia* (2). These outgroup genera are all members of the '*Pseudemoia*' group (as defined by Greer, 1989). *Lampropholis* was identified by Greer (1989) as the closest living relative to *Saproscincus*, and these two genera along with *Carlia* (and *Lygisaurus*) form a subgroup that shares a unique derived character state of the hemipenis - *Harrisoniascincus* was chosen as a distant representative that lies outside this subgroup. In the alignment of 393 bases, 277 were invariant, 7 were variable but parsimony uninformative, and 109 were informative. The Cytb dataset comprised 40 sequences from *Saproscincus* plus outgroup sequences from the genus *Lampropholis* (2), *Harrisoniascincus* (1), and

TABLE 1. Comparison of size and key scalation characters between members of the *Saproscincus* '*challengeri*' group - comparative data for *S. challengeri*, *S. spectabilis* and *S. rosei* from Sadlier et al., 1993.

	Saproscincus eungellensis	*Saproscincus challengeri*	*Saproscincus spectabilis*	*Saproscincus rosei*
Adult body length maximum SVL	67	57	59	64
Midbody scale rows range mean±sd. N	22-24 23.3 ± 0.95 13	23-26 24.6 ± 1.9 63	22-24 22.7 ± 0.9 58	22-26 24.1 ± 0.9 101
paravertebral scale rows range mean±sd. N	55-58 57.0 ± 1.0 13	54-63 57.6 ± 1.6 63	56-61 57.7 ± 1.7 58	55-67 58.8 ± 2.2 101
fourth finger scales range mean±sd. N	9-12 10.7 ± 0.5 13	9-11 10.0 ± 0.3 63	9-11 10.2 ± 0.4 57	8-11 9.7 ± 0.8 100
fourth finger lamellae range mean±sd. N	18-24 20.3 ± 1.45 13	15-19 17.3 ± 0.9 63	16-21 17.9 ± 1.0 57	14-18 15.3 ± 0.9 100
fourth toe scales range mean±sd. N	10-14 11.8 ± 0.8 13	10-13 11.2 ± 0.4 63	11-14 12.3 ± 0.9 58	10-14 11.2 ± 0.6 100
fourth toe lamellae range mean±sd. N	26-34 28.5 ± 2.2 13	23-27 24.3 ± 1.0 63	22-28 24.8 ± 1.4 58	17-24 21.0 ± 1.2 100

Carlia (2). In the alignment of 381 bases, 214 were invariant, 11 were variable but parsimony uninformative, and 156 informative.

SYSTEMATICS

Saproscincus Wells & Wellington, 1984

Saproscincus is a group of eleven species of moderately small to very small scincid lizards occurring along the tropical to temperate east coast of Australia. Greer (1989) diagnosed *Saproscincus* from its nearest living relative, *Lampropholis*, on the basis of a reduced number of labial scales (six *vs* seven) and in having a pale spot at the base of thigh. Within the genus a monophyletic group of species restricted to rainforest habitats of mid E and NE Queensland has been identified (Greer & Kluge, 1980; Greer 1989), that now comprises *S. basiliscus*; *S. tetradactyla*; *S. czechurai*; *S. hannahae* and *S. lewisi*. The remaining members of the genus fall into one of two smaller morphological groups based largely on overall similarity. The '*challengeri*' group (*S. challengeri*, *S. spectabilis*, and *S. rosei* - Sadlier et al., 1993) from moist closed forest habitats from mid E NSW to SE Queensland, and the '*mustelinus*' group, which consists of two species, *S. mustelinus* from Victoria to the N NSW highlands, and *S. oriaris* from near coastal habitats of the mid N NSW coast to the sand islands of SEQ (North Stradbroke Island, photographic record, Wildnet, EPA).

Saproscincus eungellensis sp. nov. is most similar in morphology to the species in the '*challengeri*' group. Its exceptionally large size in combination with a suite of scalation characters (see diagnoses below and Table 1) indicate it is not conspecific with any other member of the genus. This assessment of both its distinctiveness and immediate relationships is supported by the molecular data presented here and by Moussalli et al. (2005).

Saproscincus eungellensis sp. nov. (Figs 1-3)

MATERIAL EXAMINED. HOLOTYPE: QMJ76811 upper Finch Hatton Creek (21°09'S 148°38'E), 28 Nov., 2001. PARATYPES: QMJ49668 Eungella N.P. (20°55'S 148°30'E); QMJ76810 upper Finch Hatton Creek (21°09'S 148°38'E); QMJ76812 upper St Helen's Creek catchment (20°54'S 148°47'E); QMJ76813 upper Finch Hatton Creek (21°09'S 148°38'E); QMJ76814 Mt Dalrymple road near Clarke Range (21°02'S 148°38'E); QMJ79934 Mt William

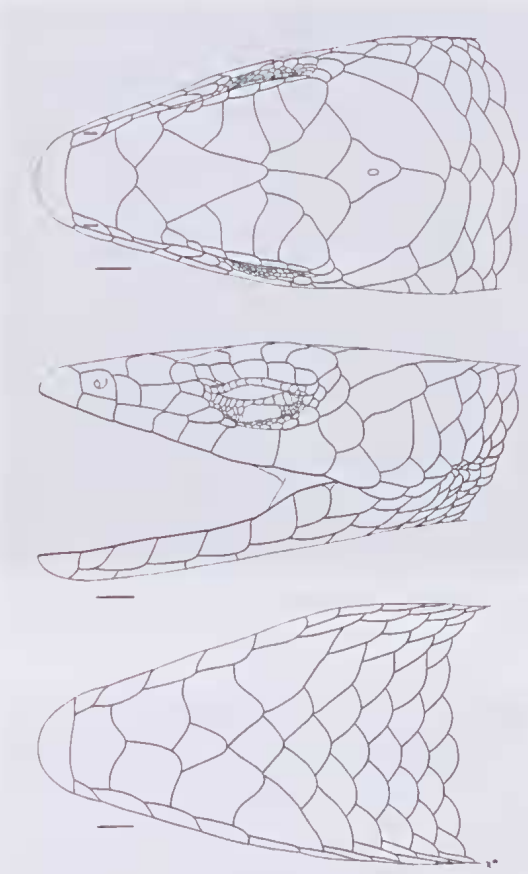

FIG. 1. Dorsal (upper), lateral (middle), and ventral (lower) views of the headshields of the holotype of *Saproscincus eungellensis* sp. nov. This specimen is atypical in having seven rather than six upper labial scales).

(21°01'40"S 148°36'15"E); QMJ78473-77 headwaters of Cattle Creek, Mt William (21°01'48"S 148°36'36"E); AMSR47495-96 Mt William via Eungella (21°01'S 148°36'E).

DIAGNOSIS. Frontoparietal scales paired and distinct from interparietal; upper labial scales six, with the fourth located under the eye; body scales smooth; limbs pentadactyl; and a dark-edged, pale spot at the base of thigh; parietal scales each bordered by a single nuchal and temporal scale; lamellae beneath the fourth toe 26-34; supraciliary scales usually six. The first five characters will identify the species described here as a member of *Saproscincus*. The sixth character will distinguish it from *S. basiliscus*; *S. tetradactyla*; *S. czechurai*; *S. hannahae* and *S. lewisi*, all of which a single nuchal and two temporal scales bordering each parietal scale The high number of lamellae beneath the fourth toe and modal number of supraciliary scales in combination will usually serve in distinguishing *S. eungellensis* from the other members of the '*challengeri*' species group (see Table 1), however no single scalation character will serve to unequivocally identify the new species from the other members of '*challengeri*' species group.

Saproscincus eungellensis is most similar to *S. challengeri* in having a modal number of six supraciliary scales, but differs in being markedly larger in adult body size for both sexes, and in having significantly more lamellae beneath the fourth toe. Sexual dimorphism in adult body colouration is more prevalent in *S. eungellensis* with the majority of adult females (70%) having a uniformly coloured unmarked dorsal surface, whereas this pattern of sexual dimorphism occurs in much lower frequencies (<20%) in *S. challengeri* (Sadlier et al., 1993).

In addition to these colour and scalation differences, the distinctiveness of the new taxon is strongly supported by DNA sequence data. Direct comparison between five individuals of *S. eungellensis* and four individuals (two each from two localities) of *S. challengeri* for the mitochondrial 12S gene shows a high level of sequence divergence between these putative species (average Kimura pairwise distances between the groups is 0.128), and no or very low levels of divergence within each population (no haplotype variation being observed in the specimens scored from either species). This level of genetic differentiation suggests the two widely allopatric populations represent two distinct evolutionary lineages.

ETYMOLOGY. From Eungella.

DESCRIPTION. Based on the type series of 14 specimens (38.0-67.0mm SVL), comprising 5 adult males, 7 adult females, 1 subadult, and 1 juvenile.

Measurements (based on adults only): maximum SVL of ♂♂ 58.0mm, ♀♀ 67.0mm; distance from axilla to groin 53.3-58.5% of SVL (= 56.4%, n = 12); hindlimb length 35.1-41.9% of SVL (= 38.1%, n=12); tail length 145.6% of SVL for adult QMJ76812 with most complete tail.

Scalation (based on adults and one subadult): prefrontals moderately large and usually

FIG. 2. *Saproscincus eungellensis* sp. nov., QMJ78612, an adult female from upper St Helens Creek –dorsal surface with scattered pale and dark markings.

moderately separated (77%), occasionally more narrowly seperated; frontoparietals paired; interparietal distinct; parietals each bordered by a single large upper secondary temporal and a pair of transversely enlarged nuchal scales, the latter occasionally separated from contacting medially (31%); nasals widely separated; loreals two; supraciliaries usually 6 (88.5%), rarely 5 (7.5%) or 7; upper labials usually 6 (81%), sometimes 7; primary temporal single; lower secondary temporal single; tertiary temporals usually single (77%), occasionally two; postlabials two; lower eyelid with an obvious, centrally located semi-transparent disc, and contacting the subocular supralabial.

Midbody scale rows 22-24 (= 23.3 ± 0.95, n = 13); paravertebral scales 55-58 (= 57.0 ± 1.00, n = 13) – no sexual dimorphism between 5 males and 7 females (56.2 *vs* 57.4, t_{10} = -2.600, P<-0.027); scales on top of fourth finger 9-12 (= 10.7 ± 0.52, n = 13); lamellae beneath fourth finger 18-24 (= 20.3 ± 1.45, n = 13); scales on top of fourth toe 10-14 (= 11.8 ± 0.78, n = 13); lamellae beneath fourth toe 26-34 (= 28.4 ± 2.20, n = 13).

Osteology: presacral vertebrae 27 (n = 11) – 28 (n =1); postsacral vertebrae 51 (QMJ79934 – juvenile specimen with complete tail with vertebrae extending to the tip); phalangeal formula for manus and pes 2.3.4.5.3 and 2.3.4.5.4 respectively.

Coloration: Adult males – dorsal surface of body and limbs mid brown with scattered paler markings (usually a single whole scale) and less frequently with finer dark flecks, the lateral surface usually becoming lighter on the side of the head and neck and towards the ventral surface. Head mid brown above (similar to body) and variably with a concentration of fine dark brown markings around the posterior edge of the parietal and frontoparietal scales. Junction of lateral and dorsal surface defined by a series of dark markings on scale row three, continuous anteriorly with a broad dark temporal streak that extends from the level of the ear opening to the nasal. Dark upper lateral markings on the body form a near continuous line along the third or fourth scale row. Ventral surface pale with fine dark brown flecks on the neck, body, and tail and either distributed evenly and forming regular (but broken) longitudinal rows over most of the body; or only as regular rows on the outer edges of the venter with sparse scattered markings centrally; or only as scattered flecks. Tail with dark brown markings along the ventrolateral margin.

Adult females – two colour forms are present, one is similar to adult males (but darker) in having scattered pale and dark markings on the dorsal surface (Fig. 2), and is represented by two adults (J76812 & J76814). The more common form has a uniform light or mid-brown dorsal

FIG. 3. *Saproscincus eungellensis* sp. nov., QMJ78610, an adult female from upper Finch Hatton Creek – uniform dorsal surface.

surface with no markings (Fig. 3), and gives the body a distinctive two-toned appearance. Lateral surface brown to grey (lighter than dorsum), defined by a dark brown dorsolateral stripe (along scale rows three and four), that is continuous with a dark temporal streak. Dark dorsolateral stripe pale edged above (1/2 scale width) that broadens significantly into a broader band (1-1.5 scales width) just posterior of the hindlimbs. Markings on underside of body and tail as in males.

Subadult and juvenile - colour pattern typical of adult males.

REPRODUCTION: Two ♀♀ (QMJ76810, QMJ76811) collected at the very end of the dry season in late November 2003 each had six shelled oviducal eggs, two other adult females (QMJ76812, QMJ76814) collected at this time had large convoluted oviducts indicating that egg-laying had already taken place in these individuals.

COMPARISON. *Saproscincus eungellensis* is readily distinguished from the 'northern' lineage (*S. basiliscus*; *S. tetradactyla*; *S. czechurai*; *S. hannahae*; and *S. lewisi*) by its much larger size (max. SVL of 49.8mm for *S. basiliscus*, largest member of the group, and 42.3mm for regionally sympatric *S. hannahae* - Couper & Keim, 1998) and in having the parietal scales each bordered by a single enlarged nuchal scale and upper secondary temporal scale (*vs* a nuchal and two upper temporal scales).

It can be distinguished from the '*mustelinus*' group (*S. mustelinus* and *S. oriaris)* in having more lamellae beneath the fourth finger (18-24 *vs* 9-14 and 13-16 respectively) and more lamellae beneath the fourth toe (26-34 *vs* 14-19 and 18-22 respectively (Sadlier, 1998, table 1).

No single scalation character will unequivocally differentiate *S. eungellensis* from the '*challengeri*' species group. The high number of lamellae beneath the fourth toe in *S. eungellensis* (26-34) is non-overlapping with *S. rosei* (17-24), almost so with *S. challengeri* (22-27), and to a lesser extent with *S. spectabilis* (22-28). Most *S. eungellensis* and *S. challengeri* have six supraciliary scales whereas *S. rosei* and *S. spectabilis* usually have seven. The large size of *S. eungellensis* will assist in distinguishing its mature individuals. Adult female *S. eungellensis* reach a maximum SVL of 67 mm (Table 1) which is 10mm longer than the largest *S. challengeri*, 8mm longer than the largest *S. galli*, and 3mm longer than the largest *S. rosei* recorded by Sadlier et al. (1993).

DISTRIBUTION AND HABITAT. *S. eungellensis* is known from five locations, all above 700 m, in the Clarke Range, mid E Queensland (Fig. 4).

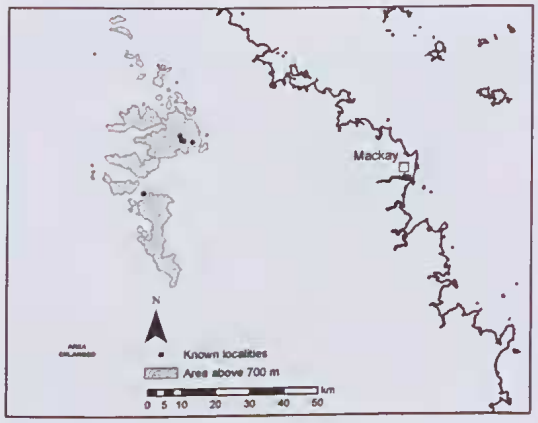

FIG. 4. Distribution map for *Saproscincus eungellensis* sp. nov. Black dots are known sites.

The upper Fineh Hatton Creek (QMJ76810-11, QMJ76813), upper St Helen's Creek (QMJ76812), and Mt. Dalrymple road (QMJ76814) speeimens were eollected from thiek rainforest in elose proximity to rainforest streams (<10 m) (Figs 5, 6). Vegetation included Water Fern (*Bleehnum cartilagineum*) and Silky Fan Fern (*Stieherus flabellatus*), both of whieh oeeur along roeky seetions of the ereek line. Alexander and/or Pieeabeen palms (*Arehontophoenix alexandrae* and *A. eunninghamiana,* respeetively) were present and the eanopy gap above the ereek was eriss-erossed with oeeasional lianas and lawyer eanes (*Calamus* sp.). In several eases the skinks were within the splash zone of riffles and waterfalls. These were often wet, either from splashing or direet immersion. They appeared to be eool and apparently had some diffieulty moving. Individuals would often allow a elose approaeh without fleeing. A single individual was seen, but not eolleeted, at the Broken River eampground (1210'10"S, 148° 30'17"E). It was among introduced, unmown lawn grasses where sunlight broke through the riparian trees. It was within 20m of a large pool. *Eulamprus amplus*, *E. luteilateralis*, and *Saproscincus hannahae* were observed in sympatry with *S. eungellensis* (habitat observations, E.V.).

CONSERVATION STATUS. Using the 'Nomination form and guidelines for listing proteeted wildlife under the *Nature Conservation Act 1992*' (Environmental Proteetion Ageney, Queensland Parks and Wildlife Serviee), *S. eungellensis* qualifies as an Endangered speeies (B2). It meets the following seleetion eriteria: 1) 'Area of oeeupaney estimated to be less than 500 km^2'; 2) 'known to exist at no more than five loeations'; 3) 'Continuing deeline...projeeted, in...area, extent and/or quality of habitat'.

The maximum area of oeeupaney was ealeulated using AreMap 8 (ESRI GIS and Mapping Software) eombined with 2002 satellite imagery (E.V.). 'Islands' of suitable habitat, above 700m, were ineluded in the ealeulation only if the long axis was greater than 1km. Using this approaeh, a total area of 498km^2 is available, but this eontains 39km^2 of eleared land and 3.5km^2 of drier woodlands (visible in the satellite imagery). Henee, the area of suitable habitat is approximately 459km^2. If *S. eungellensis* is restrieted to ereek lines, as eolleetion data and observational reeords suggest, its true distribution is eonsiderably less.

Saproscincus eungelleusis is known from five loeations: Upper Fineh Hatton Creek; Upper St Helen's Creek, Mt Dalrymple road; Mt William and the Broken River Campground (E.V., sighting only). QMJ49668 is from 'Eungella N.P.' (listed in material examined). This loeality lacks preeision and eneompasses all the above eolleetion sites. The eore habitat is eentred in the rainforests of the Mt William, Mt David and Mt Dalrymple eatehments. Two other vertebrates endemic to Eungella are narrowly restrieted to this area: *Eulamprus luteilateralis* and *Rheobatrachus vitelliuus* (K. MeDonald (EPA) pers. eomm.). *E. luteilateralis* is eonfined to altitudes above 900m (Covaeevieh & MeDonald, 1991) and *R. vitellinus* (before its disappearanee in 1985) was found above 400m (MeDonald, 1990).

It is reasonable to projeet a deeline in the quality of rainforest habitat in the Dalrymple Heights as a eonsequenee of global warming. Using projeetions of speeies' distributions for future elimate seenarios (projeeted to 2050), Thomas et al. (2004) assessed extinetion risks for a sample of 1,130 terrestrial speeies (vertebrates, invertebrates and plants) from areas from Mexieo to Australia. Even their minimum projeetions are alarming; 9-13% extinetion where species have no limits to dispersal and 22-31% where they are ineapable of dispersal. The impact of rising temperatures on plant and animal eommunities living in environmental extremes (polar and high altitude) is diseussed in a reeent popular artiele (Montaigne, 2004), aptly titled 'No Room to Run'. Extrapolating from the predietions of Thomas et al. (2004), *Saproscincus eungellensis* and a number of other Queensland reptiles (notably *Calyptotis thorntonensis, Eulamprus frerei, E. luteilateralis, E. tryoni,*

FIG. 5. Habitat of *Saproscincus eungellensis* sp. nov., Finch Hatton Creek.

Lampropholis robertsi and *Techmarscincus jigurru*) may have an elevated extinction risk. These lizards all occupy high altitude rainforest refugia and have very limited dispersal capabilities. Whether they can acclimatize to rising temperature cannot be assessed on current knowledge. It is worth noting that the *Saproscincus* spp. so far assessed for mean critical thermal maximum temperature (CTMax) (*S. hannahae* as *Lampropholis* sp. 4 in Greer 1980; *S. mustelinus* and *S. tetradactylus* as *Lampropholis* sp. 5 in Greer 1980) all have a low (CTMax) when compared to other Australian skinks (35.5, 38.6 and 35.3°C respectively; Greer, 1980, 1989).

The upward migration of low and mid altitude plant and animal species in response to global warming threatens the integrity of montane communities. In assessing the affects of climate change on mountain plants, Grabherr et al. (1994) stated that '...the warming is sufficient to stimulate migration, and may cause disastrous extinctions in these environments'.

The forested area at Dalrymple Heights has already been reduced by clearing for dairying (between 1947 and 1962; Brown, 1999) and 2,000 hectares, in State Forest 62, were logged between 1960 and 1976 (Brown, 1999). Rainforest logging totally ceased in this area in 1992 (D. Croker (DPI-Forestry) pers. comm.). 'Many of the most severe impacts of climate-change are likely to stem from interactions between threats,...' (Thomas et al., 2004) and the rainforests of Dalrymple Heights may be particularly prone to damage. In 1975, *Phytophthora cinnamomi* was identified from soil samples taken from dead patches of rainforest at Dalrymple Heights. Brown (1999) stated that 'Area calculations over the most severely affected 641 ha at Dalrymple Heights indicated that, while there were probably no deaths in 1970, by 1976 4.6% of the forest was dead. This increased to 11.9 % in 1978 and further to 19.3% (125 ha in total) in 1980'. At the time of this study, the Dalrymple Heights rainforest patch deaths were reported as '... by far the most severely affected area of rainforest seen

FIG. 6. Habitat of *Saproscincus eungellensis* sp. nov., St Helens Creek.

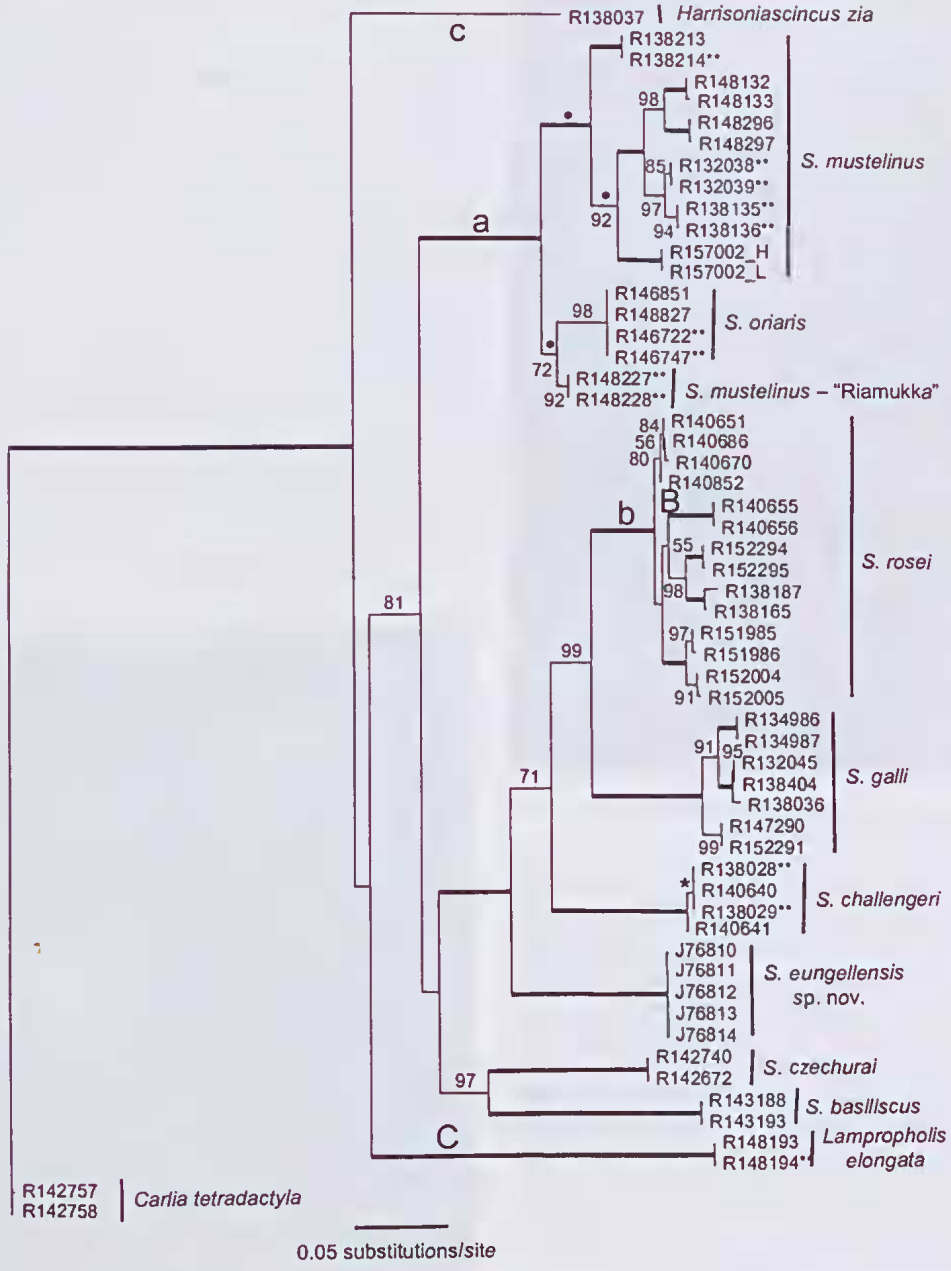

FIG. 7. One of six maximum likelihood (ML) trees for the combined data. The one branch not observed in the strict consensus of the ML trees is indicated by an asterisk. Thicker branches have a posterior probability of 100 percent in Bayesian analyses. Numbers near branches indicate posterior probabilities less than 100 but greater than 50. Thinner branches without figures have posterior probabilities less than 50. Differences from the maximum parsimony (MP) strict consensus topology are indicated. The three branches indicated by dots are not observed in the MP consensus giving a five branch polytomy at "a". Branch "B" in the ML tree is moved to "b" in the MP consensus and branch "C" in the ML tree to "c" in the MP consensus. Two tissues were sequenced from AMS R157002 as an internal control: H = heart and L = liver. Specimens not scored for CytB are indicated with a double asterisk.

from aerial observation, aerial photography and ground inspections anywhere in the tropical rainforests of Queensland' (Brown, 1999). There has been subsequent recovery (while patches of die-off are still present, they do not represent large areas when viewed from above; D. Ball (EPA) pers. comm.) but *P. cinnamomi* remains in the soil and there is evidence that both logging and feral pigs (present in Eungella NP) have played a role in its dissemination (Brown, 1999). A forest stressed by rising temperatures may be vulnerable to future *Phytophthora* outbreaks. *Phytophthora cinnamomi* is active in the soils of Eungella's rainforests during the summer (September-May) when soil temperatures are 20-21° C (Brown, 1999), however, higher temperatures (24-28° C) are optimal for hyphal growth and sporangial production (Cahill, 1999).

INTRAGENERIC RELATIONSHIPS. An independent genetic study of all species in the genus by Moussalli et al. (2005) using a combined ND4 & 16S dataset gave strong support for two clades within *Saproscincus*: a 'northern' and a 'southern' group. The 'northern' group corresponded to the monophyletic lineage of relatively small species defined morphologically by Greer (1989), while the 'southern' group included both the '*mustelinus*' and '*challengeri*' groups (with *S. eungellensis* in the latter) as sister taxa.

Our phylogenetic analysis of representatives of 8 of the 11 species in the genus using portions of the mitochondrial 12S and Cytb genes combined, and both likelihood (maximum likelihood and Bayesian) and maximum parsimony analyses, was able to identify the major groups and clearly identified the '*mustelinus*' group as the sister to the 'northern' group + '*challengeri*' group. Our analyses did identify the two 'northern' group representatives (*S. czechurai* and *S. basiliscus* as sister species, but does not provide strong support for a close relationship between these species and the '*challengeri*' group (Fig. 7).

Both Moussali et al. (2005) and this study clearly identified monophyly of the '*challengeri*' group inclusive of *S. eungellensis*, but differ in the placement of *S. eungellensis* within that clade. The combined ND4 & 16S analysis placed *S. eungellensis* as the sister taxon to the species pair *S. spectabilis* + *S. rosei*, with *S. challengeri* basal within the group. The maximum likelihood and Bayesian analyses for 12S and Cytb combined give moderate support for *S. eungellensis* as the sister taxon to all other species in the '*challengeri*' group (Fig. 7). Genetic difference between the species in the '*challengeri*' group is relatively high with average pairwise Kimura two-parameter distances of 0.128 between *S. eungellensis* and *S. challengeri* (based on 12S data only), and ranges of 0.098 to 0.105 (12S) or 0.111 to 0.143(Cytb) between populations of *S. challengeri* and *S. spectabilis* and 0.064-0.068 (12S) or 0.165 – 0.237 (Cytb) between populations *S. challengeri* and *S. rosei*. The average pairwise distances between populations of *S. spectabilis* and *S. rosei* range between 0.050 and 0.102 (12S) and 0.152 and 0.181 (Cytb). These are relatively deep divergences. Such levels of differentiation between rainforest restricted species in the Wet Tropics of northern Australia have been attributed to vicariance associated with the contraction of rainforests to isolated refugia during the Miocene and Pliocene (Schneider et al., 1998; Schneider & Moritz, 1999; Moritz et al., 2000; & Moussalli et al., 2005).

At a finer scale regional differentiation across the range of the various populations of *S. rosei* was observed, but there is little structure or indication of intrapopulation relationships. This pattern is consistent with a species that has undergone recent widespread range increases from a single source population, possibly as a result of initial contraction to a single refugium with subsequent expansion. Contraction of rainforest during the Pleistocene glacial periods and subsequent expansion during the Holocene has been proposed as the mechanism by which such patterns of low level genetic differentiation are present in now disjunct rainforest blocks in the Wet Tropics (Schneider et al., 1998; Schneider & Moritz, 1999).

Within the '*mustelinus*' group the combined 12S and Cytb ML analysis found posterior probability support of 72% for a sister group relationship between *S. oriaris* and the Riamukka population of *S. mustelinus*. The closeness of the relationship is emphasized by the fact that the Kimura two-parameter genetic distance between these groups averages 0.015 for 12S (Cytb was not scored in the Riamukka population) but ranges between 0.028 and 0.043 for comparisons of Riamukka population and other populations of *S. mustelinus*. However, *S. oriaris* and the northern Tablelands populations of *S. mustelinus* are morphologically distinct and the status of *S. oriaris* as a valid species has not been challenged since its description 5 years ago.

A similar relationship, a sister-group relationship between *S. oriaris* and a 'central' population of *S. mustelinus* (although a different sampling of localities was used) was observed by Moussalli et al (2005), and was attributed to a recent and rapid origin of *S. oriaris* from geographically adjacent populations of *S. mustelinus*.

ACKNOWLEDGEMENTS

The authors thank Derek Ball, Tanya Parker, Keith McDonald (QNPWS) and Dave Croker (DPI Forestry, Mackay) for providing information on the rainforests in the Dalrymple Heights area. Hannah Finlay produced the illustration of the head shields (Fig.1).

LITERATURE CITED

BROADBENT, J. & CLARK, S. 1976. A faunal survey of east Australian rainforests. Studies by the Australian Museum in mid-eastern and north-eastern Queensland and northern New South Wales. Interim Report. (Australian Museum: Sydney). 132p.

BROWN, B. 1999. Occurrence and impact of *Phytophthora cinnamomi* and other *Phytophthora* species in the rainforests of the wet tropics world heritage area, and of the Mackay region, Qld. Pp. 41–76. In Gadek, P.A. (ed) Patch deaths in tropical Queensland rainforest: association and impact of *Phytophthora cinnamomi* and other soil borne pathogens. (Cooperative Research Centre for Tropical Rainforest Ecology and Management, Technical Report: Cairns). 98p.

CAHILL, D. 1999. General biology and ecology of *Phytophthora* with special reference to *Phytophthora cinnamomi*. Pp. 21-26. In Gadek, P.A. (ed) Patch deaths in tropical Queensland rainforest: association and impact of *Phytophthora cinnamomi* and other soil borne pathogens. (Cooperative Research Centre for Tropical Rainforest Ecology and Management, Technical Report: Cairns). 98p.

COUPER, P.J., COVACEVICH, J.A. & MORITZ, C. 1993. A review of the leaf-tailed geckos endemic to eastern Australia: a new genus, four new species, and other new data. Memoirs of the Queensland Museum 34(1): 95-124.

COUPER, P.J. & KEIM, L.D. 1998. Two new species of *Saproscincus* (Reptilia: Scincidae) from Queensland. Memoirs of the Queensland Museum 42(2): 465-473.

COUPER, P.J., SCHNEIDER, C.J., HOSKIN, C.J. & COVACEVICH, J.A. 2000. Australian leaf-tailed geckos: phylogeny, a new genus, two new species, and other data. Memoirs of the Queensland Museum 45(2): 253-265.

COVACEVICH, J. & MCDONALD, K. R. 1991. Frogs and reptiles of tropical and subtropical eastern Australian rainforests: distribution patterns and conservation. Pp. 281-309. In Werren, G. & Kershaw, P. (eds) The rainforest legacy, Australian National Rainforests Study, volume 2 – Flora and fauna of the rainforests' (Australian Government Publishing Service: Canberra). 414p.

GRABHERR, G., GOTTFRIED, M. & PAULL, H. 1994. Climate effects on mountain plants. Nature 369: 448.

GREER, A.E. 1980. Critical thermal maximum temperatures in Australian scincid lizards: their ecologieal and evolutionary significance. Australian Journal of Zoology 28: 91-102.

1989. The biology and evolution of Australian lizards. (Surrey Beatty & Sons: Chipping Norton). 264 p.

GREER, A.E. & KLUGE, A.G. 1980. A new species of *Lampropholis* (Lacertilia: Scincidae) from the rainforests of northeastern Queensland. Occasional Papers of the Museum of Zoology University of Michigan 691: 1-11

HOSKIN, C.J., COUPER, C.J. & SCHNEIDER, C.J., 2003. A new species of *Phyllurus* (Lacertilia: Gekkonidae) and a revised phylogeny and key for the Australian leaf-tailed geckos. Australian Journal of Zoology 51: 153-164.

HUELSENBECK, J. P. & RONQUIST, F. R. 2001. MRBAYES: Bayesian inference of phylogeny. Bioinformatics 17: 754-755.

KOCHER, T.D., THOMAS, W.K., MEYER, A., EDWARDS, S.V., PÄÄBO, S., VILLA-BLANCA, F.X. & WILSON, A.C. 1989. Dynamics of mitochondrial DNA evolution in animals: Amplification and sequencing with conserved primers. Proceedings of the National Academy of Sciences 86: 6196-6200.

KUMAR, S., TAMURA, K. & NEI, M. 2004. MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. Briefings in Bioinformatics 5: 150-163

MCDONALD, K.R. 1990. *Rheobatrachus* Liem and *Taudactylus* Straughan & Lee (Anura: Leptodactylidae) in Eungella National Park, Queensland: distribution and decline. Transactions of the Royal Society of South Australia 114(4): 187-194.

MONTAIGNE, F. 2004. Ecosigns: no room to run. National Geographic Sept: 34-55.

MOUSSALLI, A., HUGALL, A.F. & MORITZ, C. 2005. A mitochondrial phylogeny of the rainforest skink genus *Saproscincus*, Wells and Wellington (1984). Molecular Phylogenetics and Evolution 34: 190-202.

MORITZ, C., PATTON, J.L., SCHNEIDER, C.J. & SMITH, T.B. 2000. Diversification of rainforest faunas: an integrated molecular approach. Annual Review of Ecology and Systematics 31: 533-563.

POSADA, D. & CRANDALL, K.A. 1998. MODELTEST: testing the model of DNA substitution. Bioinformatics 14: 817-818.

SADLIER R.A. 1998. *Saproscincus oriarus*, a new scincid lizard (Lacertilia: Scincidae) from the

north coast of New south Wales. Memoirs of the Queensland Museum 42(2): 579-583.

SADLIER, R.A., COLGAN, D.J. & SHEA, G.M. 1993. Taxonomy and distribution of the scincid lizard *Saproscincus challengeri* and related species in southeastern Australia. Memoirs of the Queensland Museum 34(1): 139-158.

SAGHAI-MAROOF, M. A., SOLIMAN, K.M., JORGENSEN, R.A. & ALLARD, R.W. 1984. Ribosomal DNA spacer length variation in barley: Mendelian inheritance, chromosomal location and population dynamics. Proceedings of the National Academy of Sciences 81: 8018-8021.

SCHNEIDER, C.J., CUNNINGHAM, M. & MORITZ, C. 1998. Comparative phylogeography of and the history of endemic vertebrates in the Wet Tropics rainforests of Australia. Molecular Ecology 7(4): 487-498.

SCHNEIDER, C.J. & MORITZ, C., 1999. Rainforest refugia and evolution in Australia's Wet Tropics. Proceedings of Royal Society of London B 266: 191-196.

SWOFFORD, D.L. 2001. PAUP*. Phylogenetic Analysis Using Parsimony (* and other methods), Version 4b10. (Sinauer Associates: Sunderland, Massachusetts).

TAYLOR, E.H. 1935. A taxonomic study of the cosmopolitan scincoid lizards of the genus *Eumeces* with an account of the distribution and relationships of its species. Science Bulletin of the University of Kansas 36(14): 642.

THOMAS, C.D., CAMERON, A., GREEN, R.E., BAKKENES, M., BEAUMONT, L.J., COLLINGHAM, Y.C., ERASMUS, B.F.N., FERREIRA DE SIQUEIRA, M., GRAINGER, A., HANNAH, L., HUGHES, L., HUNTLEY, B., VAN JAARSVELD, A.S., MIDGLEY, G.F., MILES, L., ORTEGA-HUERTA, M.A., TOWNSEND PETERSON, A., PHILLIPS, O.L. & WILLIAMS, S.E. 2004. Extinction risk from climate change. Nature 2004: 145–148.

THOMPSON, J.D., GIBSON, T.J., PLEWNIAK, F., JEANMOUGIN, F. & HIGGINS, D.G. 1997. The CLUSTAL X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Research 25: 4876-4882.

APPENDIX

Specimens used in mitochondrial DNA study with corresponding tissue numbers (in brackets) and locality data.

Carlia tetradactyla: AMSR142757 (NR2040), AMSR142758 (NR2041), Mandurama, 4.2km NE at Coombing Creek crossing, NSW, 33°38'S 149°07'E.

Harrisoniascincus zia: AMSR138037 (NR621), Border Ranges National Park, vicinity of Brindle Creek rest area, NSW, 28°22'37"S 153°03'14"E.

Lampropholis elongata: AMSR148193 (NR3749), AMSR148194 (NR3750), Riamukka State Forest, NSW, 31°19'S, 151°39'E.

Saproscincus basiliscus: AMSR143188 (NR2191), Lamb Range, Qld, 17°07'S, 145°36'E; AMSR143193 (NR2192), Lamb Range, Qld, 17°08'S, 145°36'E.

Saproscincus czechurai: AMSR142672 (NR2124), Lamb Range, Qld, 17°06'S, 145°34'E; AMSR142740 (NR2101), Lamb Range, Qld, 17°07'S, 145°36'E.

Saproscincus mustelinus: AMSR132038 (NR375), AMSR132039 (NR376), Northbridge, Tunks Park, Sydney, NSW, 33°49'S, 151°13'E; AMSR138135 (NR571), AMSR138136 (NR572), Charlestown, Newcastle, NSW, 32°58'S, 151°41'E; AMSR138213 (NR718), AMSR138214 (NR718), Styx River State Forest, Beech Lookout, NSW, 30°31'S, 152°21'E; AMSR148132 (NR2782), AMSR148133 (NR2783), Kanangra Boyd National Park at Hollanders Creek, NSW, 33°50'S, 150°02'E; AMSR148227 (NR3782), AMSR148228 (NR3783), Riamukka State Forest, NSW, 31°20'S, 151°39'E; AMSR148296 (NR3870), AMSR148297 (NR3871), Mount Wilson area, NSW, 33°29'S, 150°25'E; AMSR157002 (NR7752), Murrurundi, NSW, 31°46'S, 150°50'E.

Saproscincus eungellensis: QMJ76810-14 - see type information for localities.

Saproscincus challengeri: AMSR138028 (NR631), AMSR138029 (NR632), Mount Warning National Park, vicinity of Breakfast Creek, NSW, 28°23'S, 153°17'E; AMSR140640 (NR2000), AMSR140641 (NR2000), Cunninghams Gap, Qld, 28°03'S, 152°25'E.